

SEQUENÇE LISTING

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<130> 23611-A USA

<140> As yet unassigned

<141> 2001-06-25

<150> 60/213,653

<151> 2000-06-23

<160> 45

<170> PatentIn Ver. 2.0

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Arg Arg

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Lys Ala Pro Lys Ser Pro Ala Lys Ala Lys
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Phe Leu Arg Gly Arg Ala Tyr Gly Leu
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Arg Gly Ile Lys Glu His Val Ile Gln Asn Ala Phe Arg Lys Ala
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Ile Val Thr Asp Phe Ser Val Ile Lys
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Leu Leu Gly Arg Asn Ser Pro Glu Val
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<400> 16
Lys Leu Val Val Val Gly Ala Arg Gly Val Gly Lys Ser
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Asp Ile Leu Asp Thr Ala Gly Leu Glu Glu Tyr Ser Ala Met Arg Asp
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Gly Leu Glu Glu Tyr Ser Ala Met
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Glu Leu Val Ser Glu Phe Ser Arg Met Ala
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Glu Ala Asp Pro Thr Gly His Ser Tyr
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Leu Leu Asp Gly Thr Ala Thr Leu Arg Leu
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<211> 9
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<213> Homo sapiens
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<211> 21
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<213> Homo sapiens
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Ile Gly Cys Trp Tyr
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<211> 26
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Lys Ala Pro Lys Ser Pro Ala Lys Ala Lys
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Arg Arg
<210> 34
<211> 255
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Human/murine
      chimeric single chain binding polypeptide (C6.5
      sFv)
<400> 34
Gln Val Gln Leu Leu Gln Ser Gly Ala Glu Leu Lys Lys Pro Gly Glu
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Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met 35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cýs 85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp 100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser 115 120 125

Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ser 130 135 140

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln 145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn 165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu 180 185 190

Ile Tyr Gly His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg 210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ala Trp Asp Asp Ser Leu 225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly 245 250 255

<210> 35

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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Human/murine
      chimeric single chain binding polypeptide (C6.5
      sFv)
<400> 35
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teetgtaagg gttetggata eagetttaee agetaetgga tegeetgggt gegeeagatg 120
cccqqqaaaq gcctgqagta catggggctc atctatcctg gtgactctga caccaaatac 180
agecegteet tecaaggeea ggteaceate teagtegaea agteegteag eactgeetae 240
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qtqqqatatt gcagtagttc caactgcgca aagtggcctg aatacttcca gcattggggc 360
cagggcaccc tggtcaccgt ctcctcaggt ggaggcggtt caggcggagg tggctctggc 420
ggtggcggat cgcagtctgt gttgacgcag ccgccctcag tgtctgcggc cccaggacag 480
aaqqtcacca tctcctgctc tggaagcagc tccaacattg ggaataatta tgtatcctgg 540
taccagcage teccaggaae ageceecaaa etecteatet atggteacae caateggeee 600
gcaggggtcc ctgaccgatt ctctggctcc aagtctggca cctcagcctc cctggccatc 660
agtgggttcc ggtccgagga tgaggctgat tattactgtg cagcatggga tgacagcctg 720
agtggttggg tgttcggcgg agggaccaag ctgaccgtcc taggt
<210> 36
<211> 269
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Human/murine
      chimeric single chain binding polypeptide (C6ML3-9
      sFv')
<400> 36
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
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                                     10
                                                          15
Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
             20
                                                      30
Trp Ile Ala Trp Val Arq Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
                                                  45
         35
                             40
Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
     50
                         55
                                              60
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Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp 100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser 115 120 125

Ser Gly Gly Gly Ser Gly Gly Gly Gly Gly Gly Gly Ser 130 135 140

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln 145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn 165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu 180 185 190

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg 210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu 225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala 245 250 255

Ala Ala His His His His His Gly Gly Gly Cys 260 265

<210> 37

<211> 807

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Human/murine chimeric single chain binding polypeptide (C6ML3-9

i...i

sFv')

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<210> 38

<211> 282

<212> PRT

<213> Artificial Sequence

<220>

<400> 38

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu

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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr 20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp

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<u>L</u> i

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser 115 120 125

105

Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser 130 135

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln 155 145 150 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn 165 170

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu 185

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg 210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu 225 230 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala 245 250 255

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Ser Ser Ser Gly Ser Glu Lys Asp Glu Leu 275

<210> 39

<211> 846

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human/murine chimeric single chain binding polypeptide (C6ML-3-9sFv'-L1-KDEL)

<400> 39

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tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120 cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180 agecegteet tecaaggeea ggteaceate teagtegaca agteegteag caetgeetae 240 ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300 gtgggatatt gcagtagttc caactgcgca aagtggcctg aatacttcca gcattggggc 360 caqqqcaccc tqqtcaccgt ctcctcaggt ggaggcggtt caggcggagg tggctctggc 420 ggtggcggat cgcagtetgt gttgacgcag ccgccctcag tgtctgcggc cccaggacag 480 aaggtcacca teteetgete tggaageage tecaacattg ggaataatta tgtateetgg 540

gcaggggtcc ctgaccgatt ctctggctcc aagtctggca cctcagcctc cctggccatc 660 agtgggttcc ggtccgagga tgaggctgat tattactgtg cctcctggga ctacaccctc 720 tegggetggg tgtteggegg aggaaccaag etgacegtee taggtgegge egeacaceat 780 catcaccatc acggtggtgg cggctgcctc gagtcctcta gctctggatc cgaaaaagat 840

taccaqcaqc tcccaggaac agcccccaaa ctcctcatct atgatcacac caatcggccc 600

gaactg

<210> 40

<211> 287 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human/murine chimeric single chain binding polypeptide (C6ML3-9sFv'-L2-KDEL)

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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr 20 25

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met 35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe 55

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr 75

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys 95 85 90

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp 110 100 105

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser

Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser 130 135 140

120

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln 145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn 165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu 180 185 190

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser 195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg 210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu 225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala 245 250 255

Ala Ala His His His His His Gly Gly Gly Cys Leu Glu Ser 260 265 270

Ser Ser Ser Gly Ser Ser Ser Gly Ser Glu Lys Asp Glu Leu 275 280 285

<210> 41

<211> 861

<212> DNA

<213> Artificial Sequence

<220>

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ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt atttttgtgc gagacatgac 300 gtgggatatt gcagtagttc caactgcgca aagtggcctg aatacttcca gcattggggc 360 cagggcaccc tggtcaccgt ctcctcaggt ggaggcggtt caggcggagg tggctctggc 420 ggtggcggat cgcagtctgt gttgacgcag ccgccctcag tgtctgcggc cccaggacag 480 aaggtcacca tctcctgctc tggaagcagc tccaacattg ggaataatta tgtatcctgg 540 taccagcagc tcccaggaac agccccaaa ctcctcatct atgatcacac caatcggccc 600 gcaggggtcc ctgaccgatt ctctggctcc aagtctggca cctcagcctc cctggccatc 660 agtgggttcc ggtccgagga tgaggctgat tattactgtg cctcctggga ctacaccctc 720 tcgggctggg tgttcggcg aggaaccaag ctgaccgtcc taggtgcggc cgcacaccat 780 catcaccatc acggtgtg cgcctgcctc gagtctagca gctccggttc ctctagctct 840 ggatccgaaa aagatgaact g

<210> 42

<211> 296

<212> PRT

<213> Artificial Sequence

<220>

<400> 42

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys 85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp 100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser 115 120 125

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

140

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln 145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn 165 .170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu 180 185 190

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser
195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg 210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu 225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala 245 250 255

Ala Ala His His His His His Gly Gly Gly Cys Leu Glu Ser
260 265 270

Ser Ser Ser Gly Ser Ser Ser Gly Ser Lys Lys Ser Ala Lys Lys 275 280 285

Thr Pro Lys Lys Ala Lys Lys Pro 290 295

<210> 43

<211> 888

<212> DNA

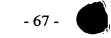
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Human/murine chimeric single chain binding polypeptide (C6ML3-9sFv'-L2-H14)

<400> 43

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ttgcaatgga gcagtctgaa gccctcggac agcgccgtgt attttgtgc gagacatgac 300 gtgggatatt gcagtagtc caactgcgca aagtggcctg aatacttcca gcattggggc 360 cagggcaccc tggtcaccgt ctcctcaggt ggaggcggtt caggcggagg tggctctggc 420 ggtggcggat cgcagtctgt gttgacgcag ccgccctcag tgtctgcggc cccaggacag 480 aaggtcacca tctcctgctc tggaagcagc tccaacattg ggaataatta tgtatcctgg 540 taccagcagc tcccaggaac agccccaaa ctcctcatct atgatcacac caatcggccc 600 gcaggggtcc ctgaccgatt ctctggctcc aagtctggca cctcagcctc cctggccatc 660 agtgggttcc ggtccgagga tgaggctgat tattactgtg cctcctggga ctacaccctc 720 tcgggctggg tgttcggcg cggctgctc gagtctagca gctccggtc ctctagctc tctagctct 840 ggatccaaga aaagcgcgaa aaagacccg aagaaagcga agaaaccg

<210> 44

<211> 291

<212> PRT

<213> Artificial Sequence

<220>

<400> 44

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
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Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Ala Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Tyr Met
35 40 45

Gly Leu Ile Tyr Pro Gly Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe

Gln Gly Gln Val Thr Ile Ser Val Asp Lys Ser Val Ser Thr Ala Tyr 65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Pro Ser Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg His Asp Val Gly Tyr Cys Ser Ser Ser Asn Cys Ala Lys Trp 100 105 110

Pro Glu Tyr Phe Gln His Trp Gly Gln Gly Thr Leu Val Thr Val Ser 115 120 125

Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser Ala Ala Pro Gly Gln 145 150 155 160

Lys Val Thr Ile Ser Cys Ser Gly Ser Ser Ser Asn Ile Gly Asn Asn 165 170 175

Tyr Val Ser Trp Tyr Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu 180 185 190

Ile Tyr Asp His Thr Asn Arg Pro Ala Gly Val Pro Asp Arg Phe Ser 195 200 205

Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu Ala Ile Ser Gly Phe Arg 210 215 220

Ser Glu Asp Glu Ala Asp Tyr Tyr Cys Ala Ser Trp Asp Tyr Thr Leu 225 230 235 240

Ser Gly Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Ala 245 250 255

Ala Ala His His His His His Gly Gly Gly Cys Leu Glu Ser 260 265 270

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Arg Lys Val 290

<210> 45

<211> 873

<212> DNA

<213> Artificial Sequence

<220>

<400> 45

caggtgcagc tggtgcagtc tggggcagag gtgaaaaagc ccggggagtc tctgaagatc 60 tcctgtaagg gttctggata cagctttacc agctactgga tcgcctgggt gcgccagatg 120 cccgggaaag gcctggagta catggggctc atctatcctg gtgactctga caccaaatac 180 agcccgtcct tccaaggcca ggtcaccatc tcagtcgaca agtccgtcag cactgcctac 240

